

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/246,129B

DATE: 10/11/2001
TIME: 14:30:50

Input Set : A:\09246129 SEQ LIST Sep 2001.txt
Output Set: N:\CRF3\10112001\I246129B.raw

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NOV 14 2001

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#21

ENTERED

p.5

2 <110> APPLICANT: Yu, Guo-Liang
3 Ni, Jian
4 Rosen, Craig A.
6 <120> TITLE OF INVENTION: Tumor Necrosis Factor Gamma
8 <130> FILE REFERENCE: PF141P4
10 <140> CURRENT APPLICATION NUMBER: 09/246,129B
11 <141> CURRENT FILING DATE: 1999-02-08
13 <150> PRIOR APPLICATION NUMBER: 60/074,047
14 <151> PRIOR FILING DATE: 1998-02-09
16 <150> PRIOR APPLICATION NUMBER: 09/131,237
17 <151> PRIOR FILING DATE: 1998-08-07
19 <150> PRIOR APPLICATION NUMBER: 09/005,020
20 <151> PRIOR FILING DATE: 1998-01-09
22 <150> PRIOR APPLICATION NUMBER: 08/461,246
23 <151> PRIOR FILING DATE: 1995-06-05
25 <150> PRIOR APPLICATION NUMBER: PCT/US94/12880
26 <151> PRIOR FILING DATE: 1994-11-07
28 <160> NUMBER OF SEQ ID NOS: 24
30 <170> SOFTWARE: PatentIn Ver. 2.0
32 <210> SEQ ID NO: 1
33 <211> LENGTH: 2442
34 <212> TYPE: DNA
35 <213> ORGANISM: Homo sapiens
37 <220> FEATURE:
38 <221> NAME/KEY: CDS
39 <222> LOCATION: (783)..(1304)
41 <220> FEATURE:
42 <221> NAME/KEY: mat_peptide
43 <222> LOCATION: (864)..(1304)
45 <220> FEATURE:
46 <221> NAME/KEY: sig_peptide
47 <222> LOCATION: (783)..(863)
49 <220> FEATURE:
50 <221> NAME/KEY: misc_feature
51 <222> LOCATION: (2265)
52 <223> OTHER INFORMATION: n equals a, t, g, or c
54 <220> FEATURE:
55 <221> NAME/KEY: misc_feature
56 <222> LOCATION: (2273)
57 <223> OTHER INFORMATION: n equals a, t, g, or c
59 <220> FEATURE:
60 <221> NAME/KEY: misc_feature
61 <222> LOCATION: (2307)
62 <223> OTHER INFORMATION: n equals a, t, g, or c
64 <220> FEATURE:
65 <221> NAME/KEY: misc_feature
66 <222> LOCATION: (2336)

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69 <220> FEATURE:
70 <221> NAME/KEY: misc_feature
71 <222> LOCATION: (2341)
72 <223> OTHER INFORMATION: n equals a, t, g, or c
74 <220> FEATURE:
75 <221> NAME/KEY: misc_feature
76 <222> LOCATION: (2379)
77 <223> OTHER INFORMATION: n equals a, t, g, or c
79 <400> SEQUENCE: 1
80 cccaatcaag agaaattcca tactatcacc agttggccga ctttccaagt ctagtgcaga 60
82 aatccaaggc acctcacacc tagagttcct atacctctga gactccagag gaaagaacaa 120
84 gacagtgcag aaggatatgt tagaaccac tgaaaaccta gaaggttgaa aaggaagcat 180
86 accctcctga cctataagaa aattttcagt ctgcaggggg atatccttgt ggcccaagac 240
88 attggtgtta tcatttgact aagaggaaat tatttgttgt gagctctgag tgaggattag 300
90 gaccaggagg atgccaaagt tctatcactt acctcatgcc tgtaagacaa gtgttttgtt 360
92 ccaattgatg aatggggaga aaacagttca gccaatcact tatgggcaca gaatggaatt 420
94 tgaaggggtc ggtgcctgcc ctgtcctac gtaaacaaga gaggcacga tgagttttat 480
96 ctgagtcatt tgggaaagga taattcttgc accaagccat tttcctaaac acagaagaat 540
98 agggggattc cttaaccttc attgttctcc aggatcatag gtctcaggat aaattaaaaa 600
100 ttttcaggtc agaccactca gtctcagaaa ggcaaagtaa tttgcccag gtcactagtc 660
102 caagatgta ttctcttga acaaagtgt atgtccagtc acatattctt cattcattcc 720
104 tccccaaagc agtttttagc tgttaggtat attcgatcac tttagtctat tttgaaaatg 780
106 at atg aga cgc ttt tta agc aaa gtc tac agt ttc cca atg aga aaa 827
107 Met Arg Arg Phe Leu Ser Lys Val Tyr Ser Phe Pro Met Arg Lys
108 -25 -20 -15
110 tta atc ctc ttt ctt gtc ttt cca gtt gtg aga caa act ccc aca cag 875
111 Leu Ile Leu Phe Leu Val Phe Pro Val Val Arg Gln Thr Pro Thr Gln
112 -10 -5 -1 1
114 cac ttt aaa aat cag ttc cca gct ctg cac tgg gaa cat gaa cta ggc 923
115 His Phe Lys Asn Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly
116 5 10 15 20
118 ctg gcc ttc acc aag aac cga atg aac tat acc aac aaa ttc ctg ctg 971
119 Leu Ala Phe Thr Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu
120 25 30 35
122 atc cca gag tcg gga gac tac ttc att tac tcc cag gtc aca ttc cgt 1019
123 Ile Pro Glu Ser Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg
124 40 45 50
126 ggg atg acc tct gag tgc agt gaa atc aga caa gca ggc cga cca aac 1067
127 Gly Met Thr Ser Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn
128 55 60 65
130 aag cca gac tcc atc act gtg gtc atc acc aag gta aca gac agc tac 1115
131 Lys Pro Asp Ser Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr
132 70 75 80
134 cct gag cca acc cag ctc ctc atg ggg acc aag tct gta tgc gaa gta 1163
135 Pro Glu Pro Thr Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val
136 85 90 95 100
138 ggt agc aac tgg ttc cag ccc atc tac ctc gga gcc atg ttc tcc ttg 1211
139 Gly Ser Asn Trp Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu

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140          105          110          115
142 caa gaa ggg gac aag cta atg gtg aac gtc agt gac atc tct ttg gtg 1259
143 Gln Glu Gly Asp Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val
144          120          125          130
146 gat tac aca aaa gaa gat aaa acc ttc ttt gga gcc ttc tta cta 1304
147 Asp Tyr Thr Lys Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
148          135          140          145
150 taggaggaga gcaaatatca ttatatgaaa gtccctctgcc accgagttcc taatttttctt 1364
152 tgttcaaata taattataac caggggtttt cttggggccg ggagtagggg gcattccaca 1424
154 gggacaacgg tttagctatg aaatttgagg ccaaaatttc acacttcatg tgccttactg 1484
156 atgagagtac taactggaaa aaggctgaag agagcaaata tattattaag atgggttgga 1544
158 ggattggcga gtttctaaat attaagacac tgatcactaa atgaatggat gatctactcg 1604
160 ggtcaggatt gaaagagaaa ttttcaaca cctccctgct atacaatggg caccagtggg 1664
162 ccagttattg ttcaatttga tcataaattt gcttcaattc aggagctttg aagggaagtcc 1724
164 aaggaaagct ctagaaaaca gtataaactt tcagaggcaa aatccttcac caatttttcc 1784
166 acatactttc atgccttgcc taaaaaaaat gaaaagagag ttggtatgtc tcatgaatgt 1844
168 tcacacagaa ggagttgggt ttcatgtcat ctacagcata tgagaaaagc taccttttctt 1904
170 ttgattatgt acacagatat ctaaaataagg aagtttgagt ttcacatgta tatcccaaat 1964
172 acaacagttg cttgtattca gtagagtttt cttgcccacc tattttgtgc tgggttctac 2024
174 cttaaccag aagacactat gaaaaacaag acagactcca ctcaaaattt atatgaacac 2084
176 cactagatac ttctgatca aacatcagtc aacatactct aaagaataac tccaagtctt 2144
178 ggccaggcgc agtggctcac acctgtaac ccaacacttt gggaggccaa ggtgggtgga 2204
180 tcatctaagg ccgggagttc aagaccagcc tgaccaacgt ggagaaaccc catctctact 2264
W--> 182 naaaatacna aattagccgg gcggtggtagc gcatggctgt aancctggct actcaggagg 2324 Erased
W--> 184 ccgaggcaga anaatttctt gaactgggga ggcagagggt gcggtgagcc cagancgcgc 2384
186 cattgcactc cagcctgggt aacaagagca aaactctgtc caaaaaaaaa aaaaaaaaaa 2442
188 <210> SEQ ID NO: 2
189 <211> LENGTH: 174
190 <212> TYPE: PRT
191 <213> ORGANISM: Homo sapiens
193 <400> SEQUENCE: 2
194 Met Arg Arg Phe Leu Ser Lys Val Tyr Ser Phe Pro Met Arg Lys Leu
195          -25          -20          -15
197 Ile Leu Phe Leu Val Phe Pro Val Val Arg Gln Thr Pro Thr Gln His
198          -10          -5          -1          1          5
200 Phe Lys Asn Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly Leu
201          10          15          20
203 Ala Phe Thr Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu Ile
204          25          30          35
206 Pro Glu Ser Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg Gly
207          40          45          50
209 Met Thr Ser Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn Lys
210          55          60          65
212 Pro Asp Ser Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr Pro
213          70          75          80          85
215 Glu Pro Thr Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val Gly
216          90          95          100
218 Ser Asn Trp Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu Gln
219          105          110          115

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221 Glu Gly Asp Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp
222      120      125      130
224 Tyr Thr Lys Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
225      135      140      145
227 <210> SEQ ID NO: 3
228 <211> LENGTH: 233
229 <212> TYPE: PRT
230 <213> ORGANISM: Homo sapiens
232 <400> SEQUENCE: 3
233 Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
234   1      5      10      15
236 Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
237      20      25      30
239 Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
240      35      40      45
242 Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Ser Pro
243      50      55      60
245 Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
246      65      70      75      80
248 Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
249      85      90      95
251 Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
252      100      105      110
254 Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
255      115      120      125
257 Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
258      130      135      140
260 Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
261      145      150      155      160
263 Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
264      165      170      175
266 Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu
267      180      185      190
269 Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
270      195      200      205
272 Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
273      210      215      220
275 Gln Val Tyr Phe Gly Ile Ile Ala Leu
276 225      230
278 <210> SEQ ID NO: 4
279 <211> LENGTH: 205
280 <212> TYPE: PRT
281 <213> ORGANISM: Homo sapiens
283 <400> SEQUENCE: 4
284 Met Thr Pro Pro Glu Arg Leu Phe Leu Pro Arg Val Cys Gly Thr Thr
285   1      5      10      15
287 Leu His Leu Leu Leu Leu Gly Leu Leu Leu Val Leu Leu Pro Gly Ala
288      20      25      30
290 Gln Gly Leu Pro Gly Val Gly Leu Thr Pro Ser Ala Ala Gln Thr Ala

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291          35          40          45
293 Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
294          50          55          60
296 Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
297 65          70          75          80
299 Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn
300          85          90          95
302 Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
303          100          105          110
305 Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala Pro Ser Ser Pro
306          115          120          125
308 Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr Pro Phe
309          130          135          140
311 His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
312 145          150          155          160
314 Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
315          165          170          175
317 Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
318          180          185          190
320 Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
321          195          200          205
323 <210> SEQ ID NO: 5
324 <211> LENGTH: 244
325 <212> TYPE: PRT
326 <213> ORGANISM: Homo sapiens
328 <400> SEQUENCE: 5
329 Met Gly Ala Leu Gly Leu Glu Gly Arg Gly Gly Arg Leu Gln Gly Arg
330 1          5          10          15
332 Gly Ser Leu Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu
333          20          25          30
335 Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro
336          35          40          45
338 Gln Asp Gln Gly Gly Leu Val Thr Glu Thr Ala Asp Pro Gly Ala Gln
339          50          55          60
341 Ala Gln Gln Gly Leu Gly Phe Gln Lys Leu Pro Glu Glu Glu Pro Glu
342 65          70          75          80
344 Thr Asp Leu Ser Pro Gly Leu Pro Ala Ala His Leu Ile Gly Ala Pro
345          85          90          95
347 Leu Lys Gly Gln Gly Leu Gly Trp Glu Thr Thr Lys Glu Gln Ala Phe
348          100          105          110
350 Leu Thr Ser Gly Thr Gln Phe Ser Asp Ala Glu Gly Leu Ala Leu Pro
351          115          120          125
353 Gln Asp Gly Leu Tyr Tyr Leu Tyr Cys Leu Val Gly Tyr Arg Gly Arg
354          130          135          140
356 Ala Pro Pro Gly Gly Gly Asp Pro Gln Gly Arg Ser Val Thr Leu Arg
357 145          150          155          160
359 Ser Ser Leu Tyr Arg Ala Gly Gly Ala Tyr Gly Pro Gly Thr Pro Glu
360          165          170          175
362 Leu Leu Leu Glu Gly Ala Glu Thr Val Thr Pro Val Leu Asp Pro Ala

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Use of n and / or Xaa has been detected in the
Sequence Listing. Review the Sequence Listing
to ensure a corresponding explanation is present
in the <220> to <223> fields of each sequence
using n or Xaa.

VERIFICATION SUMMARY

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Input Set : A:\09246129 SEQ LIST Sep 2001.txt

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L:184 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:520 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:524 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:534 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:640 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:642 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:644 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:648 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:699 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:701 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:703 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:761 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:763 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:771 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:773 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:775 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:853 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:855 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:857 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:859 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:861 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:863 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:865 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:1068 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1072 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1080 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1082 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1215 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1221 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1223 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1225 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1227 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1305 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1307 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1309 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1311 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1313 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1315 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1317 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1377 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1385 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1387 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24

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